1600

RAW SEQUENCE LISTING   DATE: 04/16/2003
PATENT APPLICATION: US/09/715,876   TIME: 16:55:53

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\04162003\I715876.raw**

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 3 <110> APPLICANT: Edwards Jr., John E., et al.
 5 <120> TITLE OF INVENTION: Pharmaceutical Compositions and Methods to Vaccinate Against
Disseminated
 6       Candidiasis.
 8 <130> FILE REFERENCE: 13361.4001
10 <140> CURRENT APPLICATION NUMBER: US 09/715,876
11 <141> CURRENT FILING DATE: 2000-11-18
13 <160> NUMBER OF SEQ ID NOS: 8
15 <170> SOFTWARE,: PatentIn version 3.0
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 33
19 <212> TYPE: DNA
20 <213> ORGANISM: Artificial sequence
22 <220> FEATURE:
23 <223> OTHER INFORMATION: PCR Primer
25 <400> SEQUENCE: 1
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29 <210> SEQ ID NO: 2
30 <211> LENGTH: 32
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial sequence
34 <220> FEATURE:
35 <223> OTHER INFORMATION: PCR Primer
37 <400> SEQUENCE: 2
38 ccgctcgagt cactaaatga acaaggacaa ta                       32
41 <210> SEQ ID NO: 3
42 <211> LENGTH: 31
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial sequence
46 <220> FEATURE:
47 <223> OTHER INFORMATION: PCR Primer
49 <400> SEQUENCE: 3
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53 <210> SEQ ID NO: 4
54 <211> LENGTH: 31
55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial sequence
58 <220> FEATURE:
59 <223> OTHER INFORMATION: PCR Primer
61 <400> SEQUENCE: 4
62 cgggatcctc actaaatgaa caaggacaat a                        31
65 <210> SEQ ID NO: 5
66 <211> LENGTH: 20
67 <212> TYPE: DNA
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ENTERED

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 68 <213> ORGANISM: Artificial sequence
 70 <220> FEATURE:
 71 <223> OTHER INFORMATION: PCR Primer
 73 <400> SEQUENCE: 5
 74 ccgtttatac catccaaatc                                        20
 77 <210> SEQ ID NO: 6
 78 <211> LENGTH: 22
 79 <212> TYPE: DNA
 80 <213> ORGANISM: Artificial sequence
 82 <220> FEATURE:
 83 <223> OTHER INFORMATION: PCR Primer
 85 <400> SEQUENCE: 6
 86 ctacatcctc caatgatata ac                          .           22
 89 <210> SEQ ID NO: 7
 90 <211> LENGTH: 3786
 91 <212> TYPE: DNA
 92 <213> ORGANISM: Candida albicans
 94 <400> SEQUENCE: 7
 95 atgcttcaac aatttacatt gttattccta tatttgtcaa ttgcaagtgc aaagacaatc    60
 97 actggtgttt ttgatagttt taattcatta acttggtcca atgctgctaa ttatgctttc   120
 99 aaagggccag gatacccaac ttggaatgct gttttgggtt ggtccttaga tggtaccagt   180
101 gccaatccag gggatacatt cacattgaat atgccatgtg tgtttaaata tactacttca   240
103 caaacatctg ttgatttaac tgccgatggt gttaaatatg ctacttgtca attttattct   300
105 ggtgaagaat tcacaacttt ttctacatta acatgtactg tgaacgacgc tttgaaatca   360
107 tccattaagg catttggtac agttactttta ccaattgcat tcaatgttgg tggaacaggt   420
109 tcatcaactg atttggaaga ttctaaatgt tttactgctg gtaccaatac agtcacattt   480
111 aatgatggtg ataaagatat ctcaattgat gttgagtttg aaaagtcaac cgttgatcca   540
113 agtgcatatt tgtatgcttc cagagttatg ccaagtctca ataaggtcac aactctttt    600
115 gtggcaccac aatgtgaaaa tggttacaca tctggtacaa tggggttctc cagtagtaac   660
117 ggtgacgttg ctattgattg ctcaaatatt catattggta tcacaaaagg attaaatgat   720
119 tggaattatc cggtttcatc tgaatcattt agttacacta aaacttgtac atctaatgga   780
121 attcagatta aatatcaaaa tgtacctgct ggttatcgtc catttattga tgcttatatt   840
123 tctgctacag atgttaacca atatacttta gcatatacca atgattatac ttgtgctggc   900
125 agtcgtctgc aaagtaaacc tttcacttta agatggactg gatacaagaa tagtgatgcc   960
127 ggatctaacg gtattgtcat tgttgctaca actagaacag ttacagacag taccactgct  1020
129 gtcactactt taccattcaa tccaagtgtt gataaaacca aaacaatcga aattttgcaa  1080
131 cctattccaa ccactaccat cacaacttca tatgttggtg tgactacttc ctatctgact  1140
133 aagactgcac caattggtga aacagctact gttattgttg atgtgccata tcatactacc  1200
135 acaactgtta ccagtgaatg gacaggaaca atcactacca ccacaactcg taccaatcca  1260
137 actgattcaa ttgacacagt ggtggtacaa gttccactgc caaatccaac tgttagtact  1320
139 actgaatatt ggtctcagtc ctttgctaca accactacag ttactgctcc tccaggtggt  1380
141 accgatactg tgattatcag agagccacca aaccatactg tcactactac tgaatattgg  1440
143 tcacaatcct ttgctactac tactactgtt actgctcctc caggtggtac tgactcagta  1500
145 attatcagag aaccaccaaa tccaactgtc actacaaccg agtattggtc tcaatccttt  1560
147 gctactacta ctacagttac tgctcctcca ggtggtactg actcagtaat tatcagagaa  1620
149 cctccaaacc caactgtcac caccactgaa tattggtccc aatcttacgc aaccacaact  1680
151 actgtgactg ctcctccagg aggcactgac tcagtaatta tcagagaacc accaaaccac  1740
153 actgtcacta ctactgaata ctggtcacaa tcatatgcca ccactaccac tgtaactgca  1800
155 ccaccaggtg gtactgacac tgttatcatt agagagccac caaaccacac tgtcactact  1860
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157 actgagtatt ggtctcaatc gtttgctact accacaactg taactggtcc accaagtggc  1920
159 actgatactg ttatcattag ggaaccacca aacccaactg tcaccactac tgaatactgg  1980
161 tctcaatcat atgcaaccac tactaccatt accgctccac ctggtgaaac tgataccgtt  2040
163 cttatcagag agccaccaaa ccatactgtc actactactg aatactggtc tcaatcatat  2100
165 gctacaacca ccactgttac tgcaccacct ggtgaaaccg ataccgttct tatcagagag  2160
167 ccaccaaacc atactgtcac tactactgaa tactggtctc aatcatatgc tacaaccacc  2220
169 actgttactg caccaccagg tggtaccgat actgttatca ttagagagcc accaaatcca  2280
171 acagttacta ctactgaata ttggtcacaa tcatttgcca caaccaccac agttactgct  2340
173 cctccaggtg gtactgacac tgtgattatc tatgaaagca tgtcaagttc aaagatttct  2400
175 acatcctcca atgatataac cagtatcatt ccatcatttt cccgtcctca ttatgtcaac  2460
177 agcacaacct ccgatttgtc aacatttgaa tcttcatcca tgaatactcc tacttctatc  2520
179 agtagtgatg gtatgttgtt gtcttctaca actttggtta ctgaatcaga aacaactaca  2580
181 gaactgattt gcagtgatgg taaagagtgt tctagattgt ccagttcttc tggtattgtc  2640
183 acaaatccag atagcaatga atcctcaatc gtaactagta ctgttcctac tgcaagtaca  2700
185 atgtctgatt cactttcttc aactgatggt attagtgcta catcttctga taatgtttca  2760
187 aaatcaggag tatcagttac aaccgaaact tctgttacaa ctattcaaac tactccaaac  2820
189 ccattatcat cttcagtgac atcattgact cagttgtctt caattccaag tgtttcagaa  2880
191 agtgaaagta aagttacatt tacaagcaat ggagacaacc aaagtggtac tcatgattca  2940
193 caatctactt ccactgaaat tgaaattgta acaaccagtt ctactaaagt tttaccacct  3000
195 gtcgtttctt ctaatactga tttgactagt gaaccaacaa ataccagaga caaccaact  3060
197 acattatcaa ctacttcaaa ctccatcact gaagatatca ccacatctca acctacaggt  3120
199 gataatggag acaatacttc atcaaccaat ccagttccaa ctgtggcaac aagtacttta  3180
201 gcatctgcaa gtgaagaaga caacaaaagc ggttctcatg aatcagcatc cacaagtttg  3240
203 aaaccaagta tgggtgaaaa ttctggatta actacttcta ctgaaattga agctacaaca  3300
205 accagtccta cagaagctcc atcacctgct gtttcttctg gtactgatgt aactactgaa  3360
207 ccaactgata ctagagaaca acctactaca ttatcaacta cttcaaaaac aaacagtgaa  3420
209 ctggttgcta ctacacaagc tactaatgaa aatggtggta aatctccatc aacttgattta  3480
211 acatcaagct tgacaacagg cacctcagca tctacaagtc ctaatagcaa acttgttact  3540
213 agtggatctg ttactggtgg agctgttgcc agtgcttcaa atgatcaatc acattctact  3600
215 tctgttacca acagcaacag cattgtatct aataccccac aaactacatt gagtcaacaa  3660
217 gttacctcat cctcaccttc aaccaacaca ttcattgctt ctacatacga tggctctggt  3720
219 tctattatcc aacattctac ttggttgtac ggtttgatca cattattgtc cttgttcatt  3780
221 tagtga                                                             3786
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224 <210> SEQ ID NO: 8
225 <211> LENGTH: 1260
226 <212> TYPE: PRT
227 <213> ORGANISM: Candida albicans
229 <400> SEQUENCE: 8
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232 1               5                   10                  15
234 Ala Lys Thr Ile Thr Gly Val Phe Asp Ser Phe Asn Ser Leu Thr Trp
235             20                  25                  30
237 Ser Asn Ala Ala Asn Tyr Ala Phe Lys Gly Pro Gly Tyr Pro Thr Trp
238             35                  40                  45
240 Asn Ala Val Leu Gly Trp Ser Leu Asp Gly Thr Ser Ala Asn Pro Gly
241         50                  55                  60
243 Asp Thr Phe Thr Leu Asn Met Pro Cys Val Phe Lys Tyr Thr Thr Ser
244 65                  70                  75                  80
246 Gln Thr Ser Val Asp Leu Thr Ala Asp Gly Val Lys Tyr Ala Thr Cys
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247                   85                  90                  95
249 Gln Phe Tyr Ser Gly Glu Glu Phe Thr Thr Phe Ser Thr Leu Thr Cys
250               100                 105                 110
252 Thr Val Asn Asp Ala Leu Lys Ser Ser Ile Lys Ala Phe Gly Thr Val
253               115                 120                 125
255 Thr Leu Pro Ile Ala Phe Asn Val Gly Gly Thr Gly Ser Ser Thr Asp
256        130                 135                 140
258 Leu Glu Asp Ser Lys Cys Phe Thr Ala Gly Thr Asn Thr Val Thr Phe
259 145               150                 155                 160
261 Asn Asp Gly Asp Lys Asp Ile Ser Ile Asp Val Glu Phe Glu Lys Ser
262               165                 170                 175
264 Thr Val Asp Pro Ser Ala Tyr Leu Tyr Ala Ser Arg Val Met Pro Ser
265               180                 185                 190
267 Leu Asn Lys Val Thr Thr Leu Phe Val Ala Pro Gln Cys Glu Asn Gly
268        195                 200                 205
270 Tyr Thr Ser Gly Thr Met Gly Phe Ser Ser Ser Asn Gly Asp Val Ala
271        210                 215                 220
273 Ile Asp Cys Ser Asn Ile His Ile Gly Ile Thr Lys Gly Leu Asn Asp
274 225               230                 235                 240
276 Trp Asn Tyr Pro Val Ser Ser Glu Ser Phe Ser Tyr Thr Lys Thr Cys
277               245                 250                 255
279 Thr Ser Asn Gly Ile Gln Ile Lys Tyr Gln Asn Val Pro Ala Gly Tyr
280               260                 265                 270
282 Arg Pro Phe Ile Asp Ala Tyr Ile Ser Ala Thr Asp Val Asn Gln Tyr
283        275                 280                 285
285 Thr Leu Ala Tyr Thr Asn Asp Tyr Thr Cys Ala Gly Ser Arg Leu Gln
286        290                 295                 300
288 Ser Lys Pro Phe Thr Leu Arg Trp Thr Gly Tyr Lys Asn Ser Asp Ala
289 305               310                 315                 320
291 Gly Ser Asn Gly Ile Val Ile Val Ala Thr Thr Arg Thr Val Thr Asp
292               325                 330                 335
294 Ser Thr Thr Ala Val Thr Thr Leu Pro Phe Asn Pro Ser Val Asp Lys
295               340                 345                 350
297 Thr Lys Thr Ile Glu Ile Leu Gln Pro Ile Pro Thr Thr Thr Ile Thr
298        355                 360                 365
300 Thr Ser Tyr Val Gly Val Thr Thr Ser Tyr Leu Thr Lys Thr Ala Pro
301        370                 375                 380
303 Ile Gly Glu Thr Ala Thr Val Ile Val Asp Val Pro Tyr His Thr Thr
304 385               390                 395                 400
306 Thr Thr Val Thr Ser Glu Trp Thr Gly Thr Ile Thr Thr Thr Thr Thr
307               405                 410                 415
309 Arg Thr Asn Pro Thr Asp Ser Ile Asp Thr Val Val Val Gln Val Pro
310               420                 425                 430
312 Leu Pro Asn Pro Thr Val Ser Thr Thr Glu Tyr Trp Ser Gln Ser Phe
313        435                 440                 445
315 Ala Thr Thr Thr Thr Val Thr Ala Pro Pro Gly Gly Thr Asp Thr Val
316        450                 455                 460
318 Ile Ile Arg Glu Pro Pro Asn His Thr Val Thr Thr Thr Glu Tyr Trp
319 465               470                 475                 480
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321 Ser Gln Ser Phe Ala Thr Thr Thr Thr Val Thr Ala Pro Pro Gly Gly
322             485             490             495
324 Thr Asp Ser Val Ile Ile Arg Glu Pro Pro Asn Pro Thr Val Thr Thr
325             500             505             510
327 Thr Glu Tyr Trp Ser Gln Ser Phe Ala Thr Thr Thr Thr Val Thr Ala
328         515             520             525
330 Pro Pro Gly Gly Thr Asp Ser Val Ile Ile Arg Glu Pro Pro Asn Pro
331     530             535             540
333 Thr Val Thr Thr Thr Glu Tyr Trp Ser Gln Ser Tyr Ala Thr Thr Thr
334 545             550             555             560
336 Thr Val Thr Ala Pro Pro Gly Gly Thr Asp Ser Val Ile Ile Arg Glu
337             565             570             575
339 Pro Pro Asn His Thr Val Thr Thr Thr Glu Tyr Trp Ser Gln Ser Tyr
340             580             585             590
342 Ala Thr Thr Thr Thr Val Thr Ala Pro Pro Gly Gly Thr Asp Thr Val
343         595             600             605
345 Ile Ile Arg Glu Pro Pro Asn His Thr Val Thr Thr Thr Glu Tyr Trp
346     610             615             620
348 Ser Gln Ser Phe Ala Thr Thr Thr Thr Val Thr Gly Pro Pro Ser Gly
349 625             630             635             640
351 Thr Asp Thr Val Ile Ile Arg Glu Pro Pro Asn Pro Thr Val Thr Thr
352             645             650             655
354 Thr Glu Tyr Trp Ser Gln Ser Tyr Ala Thr Thr Thr Thr Ile Thr Ala
355         660             665             670
357 Pro Pro Gly Glu Thr Asp Thr Val Leu Ile Arg Glu Pro Pro Asn His
358     675             680             685
360 Thr Val Thr Thr Thr Glu Tyr Trp Ser Gln Ser Tyr Ala Thr Thr Thr
361     690             695             700
363 Thr Val Thr Ala Pro Pro Gly Glu Thr Asp Thr Val Leu Ile Arg Glu
364 705             710             715             720
366 Pro Pro Asn His Thr Val Thr Thr Thr Glu Tyr Trp Ser Gln Ser Tyr
367             725             730             735
369 Ala Thr Thr Thr Thr Val Thr Ala Pro Pro Gly Gly Thr Asp Thr Val
370             740             745             750
372 Ile Ile Arg Glu Pro Pro Asn Pro Thr Val Thr Thr Thr Glu Tyr Trp
373         755             760             765
375 Ser Gln Ser Phe Ala Thr Thr Thr Thr Val Thr Ala Pro Pro Gly Gly
376     770             775             780
378 Thr Asp Thr Val Ile Ile Tyr Glu Ser Met Ser Ser Ser Lys Ile Ser
379 785             790             795             800
381 Thr Ser Ser Asn Asp Ile Thr Ser Ile Ile Pro Ser Phe Ser Arg Pro
382             805             810             815
384 His Tyr Val Asn Ser Thr Thr Ser Asp Leu Ser Thr Phe Glu Ser Ser
385             820             825             830
387 Ser Met Asn Thr Pro Thr Ser Ile Ser Ser Asp Gly Met Leu Leu Ser
388         835             840             845
390 Ser Thr Thr Leu Val Thr Glu Ser Glu Thr Thr Thr Glu Leu Ile Cys
391     850             855             860
393 Ser Asp Gly Lys Glu Cys Ser Arg Leu Ser Ser Ser Ser Gly Ile Val
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 04/16/2003
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Input Set : A:\EP.txt
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Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

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